

[illegible]

	9	18	27	36	45	54
5'	C CGC TGC AGC CGC TTT CTG CGG CCT GGG CCT CTC GTG GCC ATG CCA CAC				M P H	
	63	72	81	90	99	108
GCC TTC AAG CCC GGG GAC TTG GTG TTC GCT AAG ATG AAG GGC TAC CCT CAC TGG A F K K P G D L V F A K M K G Y P H W						
	117	126	135	144	153	162
CCT GCC AGG ATC GAC GAC ATC GCG GAT GGC GCC GTG AAG CCC CCA CCC AAC AAG P A R I D D I A A D G A V K P P P N K						
	171	180	189	198	207	216
TAC CCC ATC TTT TTC TTT GGC ACA CAC GAA ACA GCC TTC CTG GGC CCC AAA GAC Y P I I F F F G T G T H E T A F L G P K D						
	225	234	243	252	261	270
CTC TTC CCT TAC GAG GAA TCC AAG GAG AAG TTT GGC AAG CCC AAC AAC AGG AGG AAA L F P P Y E E S K E E K F G G K P N K R K						
	279	288	297	306	315	324
GGG TTC AGC GAG GGG CTG TGG GAG ATC GAG AAC AAC CCT ACT GTC AAG GCT TCC G F S S E G L W E I E N N P T V K A S						
	333	342	351	360	369	378
GGC TAT CAG TCC TCC CAG AAA AAG AGC TGT GTG GAA GAG CCT GAA CCA GAG CCC G Y Q S S S Q K K K S C V E E P E P E P						

FIGURE 1A

Station	Time	Lat	Long	Alt	Temp	Hum	Wind	Dir	Speed	Pressure	Clouds	Remarks
101	0000	33° 45' N	118° 05' W	10	10.0	100	0	0	0	1013.2	0	Clear
102	0100	33° 45' N	118° 05' W	10	10.0	100	0	0	0	1013.2	0	Clear
103	0200	33° 45' N	118° 05' W	10	10.0	100	0	0	0	1013.2	0	Clear
104	0300	33° 45' N	118° 05' W	10	10.0	100	0	0	0	1013.2	0	Clear
105	0400	33° 45' N	118° 05' W	10	10.0	100	0	0	0	1013.2	0	Clear
106	0500	33° 45' N	118° 05' W	10	10.0	100	0	0	0	1013.2	0	Clear
107	0600	33° 45' N	118° 05' W	10	10.0	100	0	0	0	1013.2	0	Clear
108	0700	33° 45' N	118° 05' W	10	10.0	100	0	0	0	1013.2	0	Clear
109	0800	33° 45' N	118° 05' W	10	10.0	100	0	0	0	1013.2	0	Clear
110	0900	33° 45' N	118° 05' W	10	10.0	100	0	0	0	1013.2	0	Clear
111	1000	33° 45' N	118° 05' W	10	10.0	100	0	0	0	1013.2	0	Clear
112	1100	33° 45' N	118° 05' W	10	10.0	100	0	0	0	1013.2	0	Clear
113	1200	33° 45' N	118° 05' W	10	10.0	100	0	0	0	1013.2	0	Clear
114	1300	33° 45' N	118° 05' W	10	10.0	100	0	0	0	1013.2	0	Clear
115	1400	33° 45' N	118° 05' W	10	10.0	100	0	0	0	1013.2	0	Clear
116	1500	33° 45' N	118° 05' W	10	10.0	100	0	0	0	1013.2	0	Clear
117	1600	33° 45' N	118° 05' W	10	10.0	100	0	0	0	1013.2	0	Clear
118	1700	33° 45' N	118° 05' W	10	10.0	100	0	0	0	1013.2	0	Clear
119	1800	33° 45' N	118° 05' W	10	10.0	100	0	0	0	1013.2	0	Clear
120	1900	33° 45' N	118° 05' W	10	10.0	100	0	0	0	1013.2	0	Clear
121	2000	33° 45' N	118° 05' W	10	10.0	100	0	0	0	1013.2	0	Clear
122	2100	33° 45' N	118° 05' W	10	10.0	100	0	0	0	1013.2	0	Clear
123	2200	33° 45' N	118° 05' W	10	10.0	100	0	0	0	1013.2	0	Clear
124	2300	33° 45' N	118° 05' W	10	10.0	100	0	0	0	1013.2	0	Clear
125	0000	33° 45' N	118° 05' W	10	10.0	100	0	0	0	1013.2	0	Clear

387	396	405	414	423	432
GAA GCT GCA GAG GGT GAC GGT GAT AAG AAG GGG AAT GCA GAG GGC AGC AGC GAC	E A A E G D G D K K K G N A E G S S D				
441	450	459	468	477	486
GAG GAA GGG AAG CTG GTC ATT GAT GAG CCA GCC AAG GAG AAG AAC GAG AAA GGA	E E G K L V I D E P A K E K N E K G				
495	504	513	522	531	540
GCG TTG AAG AGG AGA GCA GGG GAC TTG CTG GAG GAC TCT CCT AAA CGT CCC AAG	A L K R R A G A G D L L E D S P K R P K				
549	558	567	576	585	594
GAG GCA GAA AAC CCT GAA GGA GAG GAG AAG GAG GCA GCC ACC TTG GAG GTT GAG	E A E N P E G G E E K E A A T L E V E				
603	612	621	630	639	648
AGG CCC CTT CCT ATG GAG GTG GAA AAG AAT AGC ACC CCC TCT GAG CCC GGC TCT	R P L P M E V E E K N S T P S E P G S				
657	666	675	684	693	702
GGC CGG GGG CCT CCC CNN NNN NNN NNN NNN NNN NNN NNN NAG GAA GAG GCT	G R G G P P X X X X X X X X X X E E A				
711	720	729	738	747	756
ACC AAG GAA GAT GCT GAG GCC CCA GGC ATC AAG AGT CAT GAG AGC CTG TAG CCA	T K E E D A E A P G I K S H E S L				

FIGURE 1B

# Figure 1C

765	774	783	792	801	810
CCA ATG TTT CAA GAG GAG CCC CCA CCC TGT TCC TGC TGC TGT CTG GGT GCT ACT					
819	828	837	846	855	864
GGG GAA ACT GGC CAT GGG CTG CAA ACT GGG NAC CCC TTT TCC ANC NCA ANC TGN					

TNT TCT T 3'

FIGURE 1C

1 M P H A - - - - F K P G D L V F A K M K G Y P H W P A R I D D I A D G A V K P 876242  
1 M S R S N R Q K E Y K C G D L V F A K M K G Y P H W P A R I D E M P E A A V K S GI 598956  
1 M S R S N R Q K E Y K C G D L V F A K M K G Y P H W P A R I D E M P E A A V K S GI 945419

36 P P N K Y P I F F F G T H E T A F L G P K D L F P Y E E S K E K F G K P N K R K 876242  
41 T A N K Y Q V F F F G T H E T A F L G P K D L F P Y E E S K E K F G K P N K R K GI 598956  
41 T A N K Y Q V F F F G T H E T A F L G P K D L F P Y E E S K E K F G K P N K R K GI 945419

76 G F S E G L W E I E N N P T V K A S G Y Q S S Q K K S C V E E P E P E P E A A E 876242  
81 G F S E G L W E I E N N P T V K A S G Y Q S S Q K K S C V E E P E P E P E A A E GI 598956  
81 G F S E G L W E I E N N P T V K A S G Y Q S S Q K K S C A A E P E V E P E A H E GI 945419

116 G D G D K K G N A E G S S D E E G K L V I D E P A K E K N E K G A L K R R A G D 876242  
121 G D G D K K G N A E G S S D E E G K L V I D E P A K E K N E K G A L K R R A G D GI 598956  
121 G D G D K K G S A E G S S D E E G K L V I D E P A K E K N E K G T L K R R A G D GI 945419

156 L L E D S P K R P K E A E N P E G E E K E A A T L E V E R P L P M E V E K N S T 876242  
161 L L E D S P K R P K E A E N P E G E E K E A A T L E V E R P L P M E V E K N S T GI 598956  
161 V L E D S P K R P K E S G D H E E D K E I A A L E G E R H L P V E V E K N S T GI 945419

196 P S E P G S G R G P P X X X X X X X X X E E A T K E D A E A P G I K S H E S L 876242  
201 P S E P G S G R G P P Q E E E E E E D E E E E A T K E D A E A P G I R D H E S L GI 598956  
201 P S E P D S G Q G P P A E E E E E G E - - - E E A A K E E A E A P G V R D H E S L GI 945419

FIGURE 2

# Figure 3A: Sequence

1 CCGCTGCCAGCCGCTTTCTGCGGCCCTGGGCCCTCTCGCCGTC n876242  
 1 ATGTCGCA-----TCAACCGGC g598956  
 41 AGCATTGCCACACGCCCTTCAAGCCCGGGGACCTTGGGTGTTTCG n876242  
 20 AGAAGA-GTAC-----AAATGCGGGGACCTGGGTGTTTCG g598956  
 81 CTAAAGATGAAGGGCTACCCCTCACTGGCCCTGCCAGGATCTGA n876242  
 53 CCAAAGATGAAGGGCTACCCCAACTGGCCGGGATCTGA g598956  
 121 CGACATCGCGGATGGCGCTGGTAAGCCCCCAACCAAG n876242  
 93 CGAGATGCTGAGCTGGCGCTGAATCAACCAAG n876242  
 161 TACCCCATCTTTTCTTTTGGCAACACGAACAAGCCTTTC n876242  
 133 TACCAAGTCTTTTTTTGGGACCCACGAAGACGGCATTTC g598956  
 201 TGGGCCCAAGACCTCTTCCCTTACGAGGAATCCAAGGA n876242  
 173 TGGGCCCAAGACCTCTTCCCTTACGAGGAATCCAAGGA g598956  
 241 GAAAGTTTGGCAAGCCCAACAAGAGGAAGGTTTCAAGCAG n876242  
 213 GAAAGTTTGGCAAGCCCAACAAGAGGAAGGTTTCAAGCAG g598956  
 281 GGGCTGTGGGAGATCGAGAACAAACCTACTGTCAAGGCTT n876242  
 253 GGGCTGTGGGAGATCGAGAACAAACCTACTGTCAAGGCTT g598956  
 321 CCGGCTATCAGTCCCTCCAGAAAGAGCTGTGTGAAGA n876242  
 293 CCGGCTATCAGTCCCTCCAGAAAGAGCTGTGTGAAGA g598956

FIGURE 3A

# Figure 3B

361 G C C T G A A C C A G A G C C C G A A G C T G C A G A G G T G A C G G T G A T n876242  
 333 G C C T G A A C C A G A G C C C G A A G C T G C A G A G G T G A C G G T G A T g598956  
  
 401 A A G A A G G G G A A T G C A G A G G G C A G C A G C G A C G A G G A A G G G A n876242  
 373 A A G A A G G G G A A T G C A G A G G G C A G C A G C G A C G A G G A A G G G A g598956  
  
 441 A G C T G G T C A T T G A T G A G C C C A G C C A A G G A G A A C G A G A A n876242  
 413 A G C T G G T C A T T G A T G A G C C C A G C C A A G G A G A A C G A G A A g598956  
  
 481 A G G A G C C G T T G A A G A G G A G A G C A G G G A C T T G C T G G A G A C n876242  
 453 A G G A G C C G T T G A A G A G G A G A G C A G G G A C T T G C T G G A G A C g598956  
  
 521 T C T C C T A A A C G T C C C A A G G A G G C A G A A A C C C T G A A G G A G n876242  
 493 T C T C C T A A A C G T C C C A A G G A G G C A G A A A C C C T G A A G G A G g598956  
  
 561 A G G A G A A G G A G G C A G C C A C C T T G G A G G T T G A G A G C C C C T n876242  
 533 A G G A G A A G G A G G C A G C C A C C T T G G A G G T T G A G A G C C C C T g598956  
  
 601 T C C T A T G G A G G T G G A A A A G A A T A G C A C C C C C T C T G A G C C C n876242  
 573 T C C T A T G G A G G T G G A A A A G A A T A G C A C C C C C T C T G A G C C C g598956  
  
 641 G G C T C T G G C C G G G G G C C T C C C C C N N N N N N N N N N N N n876242  
 613 G G C T C T G G C C G G G G G C C T C C C C C A A G A G G A A G A A G A A G A G g598956

FIGURE 3B

# Figure 3C

681 NNNNNNNNAGGAAGAGGCTACCAAGGAAGATGCTGAGGC n876242  
653 AGGATGAAGAGGAAGGCTACCAAGGAAGATGCTGAGGC g598956

721 CCAGGCATCAAGAGTCAATGAGAGCCCTGTAGCCACCAATG n876242  
693 CCAGGCATCAAGAGTCAATGAGAGCCCTGTAG g598956

761 TTCAAGAGGAGCCCCCCTGTTCTCTGCTGCTG n876242  
723 g598956

801 GTGCTACTGGGGGAAACTGGGCCATGGGCTGCACCACTGGGNA n876242  
723 g598956

841 CCCCCCTTTCCANCNCANCTGNTNTCTT n876242  
723 g598956

FIGURE 3C

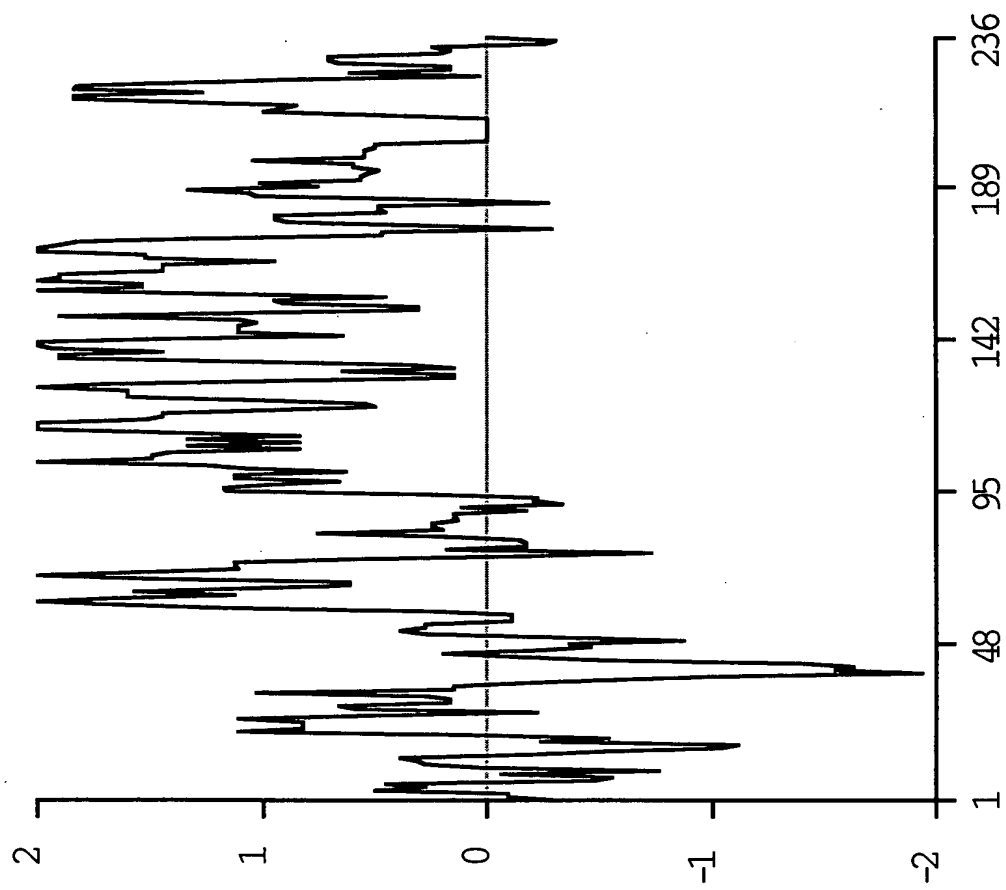
[illegible]

FIGURE 4A



04280" 9988660

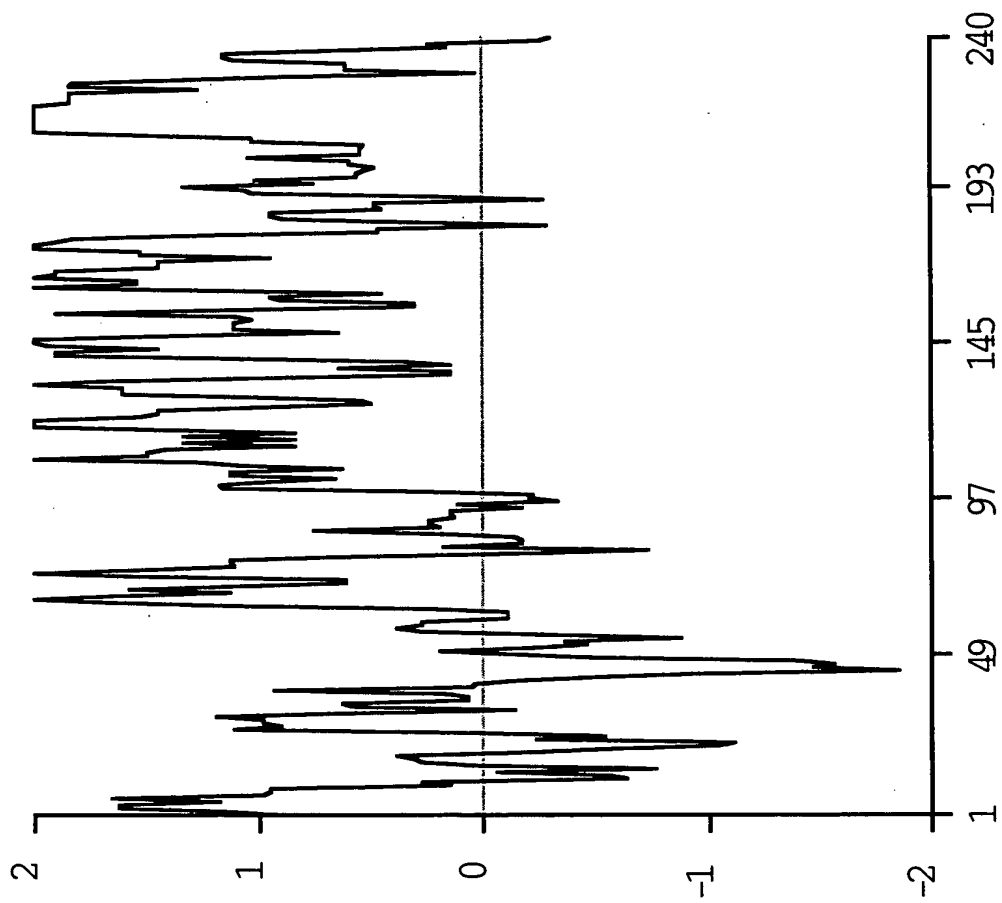


FIGURE 4B

Library	Lib Description	Abun	Pct Abun
HNT3AZT01	hNT2 cell line, teratocarcinoma, treated AZ	5	0.3425
THP1PLB02	THP-1 promonocyte cell line, treated PMA, LPS	4	0.1630
THP1PEB01	THP-1 promonocyte cell line, treated PMA	3	0.1463
PANCDIT03	pancreas, NIDDM, 57 M	1	0.1462
THP1T7T01	THP1 cells, untreated	3	0.1447
BSTMNOT01	brain stem, 72 M	1	0.1214
PROSTUT12	prostate tumor, 65 M, match to PROSNOT20	4	0.1118
HUVESTB01	HUVEC endothelial cell line, shear stress	3	0.1078
PENITUT01	penis tumor, carcinoma, 64 M	4	0.1066
AMLBNOT01	AML blast cells, blast crisis, 58 F	1	0.1058
COLNNOT13	colon, ascending, 28 M	3	0.0932
HUVENOB01	HUVEC endothelial cell line, control	2	0.0841
UTRSNOT05	uterus, 45 F	3	0.0834
SINTNOT13	small intestine, ileum, ulcerative cholangitis, 25 F	3	0.0826
LUNGNOT03	lung tumor, 69 M, match to LUNGNOT15	5	0.0796
OVARNOT01	ovary, 49 F, WM	1	0.0752
PLACNOT02	placenta, neonatal F, NORM, WM	13	0.0722
PROSNOT01	prostate, 78 M	2	0.0702
SPLNFEM01	spleen, fetal, WM	2	0.0663
COLNNOT19	large intestine, cecum, 18 F	2	0.0585
PROSTUT05	prostate tumor, 69 M, match to PROSNOT07	4	0.0580
COLNFET02	colon, fetal F	4	0.0571

FIGURE 5A

THP1NOT01	THP1 cells, untreated	1	0.0571
LUNGNOT02	lung tumor, metastasis, 79 M, match to LUNGNOT03	3	0.0567
SININOT01	small intestine, ileum, 4 F	2	0.0560
THP1AZT01	THP-1 promonocyte cell line, treated AZ	1	0.0554
LUNGNOT15	lung, 69 M, match to LUNGNOT03	2	0.0553
LIVRFET02	liver, fetal F	2	0.0550
KERANOT02	keratinocytes, primary cell line, 30 F	3	0.0546
PROSTUT09	prostate tumor, 66 M	2	0.0529
LEUKNOT03	white blood cells, 27 F	2	0.0523
TESTNOT03	testis, 37 M	4	0.0515
COLNPOT01	colon polyp, 40 F	2	0.0513
PROSNOT14	prostate, 60 M, match to PROSTUT08	2	0.0512
BRAITUT02	brain tumor, metastasis, 58 M	3	0.0509
BRSTTUT03	breast tumor, 58 F, match to BRSTNOT05	5	0.0493
TESTNOT01	testis, 37 M	1	0.0478
UCMCNOT02	mononuclear cells	2	0.0471
THP1PLB01	THP-1 promonocyte cell line, treated PMA, LPS	1	0.0452
BRSTNOT02	breast, 55 F, match to BRSTTUT01	4	0.0443
PROSNOT02	prostate, 50 M, match to PROSTUT01	1	0.0435
COLNNOT08	colon, 60 M	1	0.0426
PANCTUT02	pancreatic tumor, carcinoma, 45 F	2	0.0403
SCORNOT01	spinal cord, 71 M	2	0.0402
UTRSNOT01	uterus, 59 F	1	0.0394
SINTTUT01	small intestine tumor, ileum, 42 M	1	0.0382

FIGURE 5B

TYMNOT01	lymphocytes (non-adher PBMNC), 24 M, RP	1	0.0379
HNT2RAT01	hNT2 cell line, teratocarcinoma, treated RA	2	0.0376
BRAINOT03	brain, 26 M	2	0.0371
LUNGNOT04	lung, 2 M	2	0.0366
PROSNOT20	prostate, 65 M, match to PROSTUT12	1	0.0336
CARDFEM01	heart, fetal, NORM, WM	3	0.0335
OVARTUT01	ovarian tumor, 43 F, match to OVARNOT03	1	0.0323
OVARNOT02	ovary, 59 F	1	0.0316
NEUTGMT01	granulocytes, periph blood, M/F, treated GM-CSF	2	0.0313
BRSTNOT05	breast, 58 F, match to BRSTTUT03	2	0.0309
STOMNOT02	stomach, 52 M, match to STOMTUT01	1	0.0308
BRSTNOT07	breast, 43 F	1	0.0307
STOMNOT01	stomach, 55 M	1	0.0303
LUNGNOT18	lung, 66 F	1	0.0298
TONGTUT01	tongue tumor, carcinoma, 36 M	1	0.0295
BRAITUT08	brain tumor, astrocytoma, 47 M	2	0.0293
COLNTUT06	large intestine, cecal tumor, 45 F	1	0.0293
LIVSFEM02	liver/spleen, fetal M, NORM, WM	11	0.0290
BEPINOT01	bronchial epithelium, primary cell line, 54 M	2	0.0289
PANCNOT07	pancreas, fetal M	1	0.0287
UTRSNOT06	uterus, myometrium, 50 F	1	0.0282
LUNGNOT12	lung, 78 M	1	0.0278
TESTTUT02	testicular tumor, 31 M	1	0.0278

FIGURE 5C

THYRTUT03	thyroid tumor, benign, 17 M	1	0.0276
LARTUT02	heart tumor, myoma, 43 M	2	0.0275
BEPINON01	bronchial epithelium, 1° cell line, 54 M, NORM	1	0.0274
OVARNOT07	ovary, 28 F	1	0.0269
PTHYTUM01	parathyroid tumor, adenoma, M/F, NORM, WM	1	0.0268
KIDNTUT01	kidney tumor, Wilms, 8m F	1	0.0267
LATRNOT01	heart, left atrium, 51 F	1	0.0266
PROSTUT08	prostate tumor, 60 M, match to PROSNOT14	1	0.0266
BRSTNOM01	breast, F, NORM, WM	1	0.0264
BRAITUT13	brain tumor, meningioma, 68 M	1	0.0262
DUODNOT02	small intestine, duodenum, 8 F	1	0.0262
URETTUT01	ureter tumor, 69 M	1	0.0262
BRAITUT07	brain tumor, left frontal, 32 M	1	0.0259
LIVRTUT01	liver tumor, metastasis, 51 F	1	0.0259
PROSNOT18	prostate, 58 M	1	0.0256
PANCNOT08	pancreas, 65 F, match to PANCTUT01	1	0.0254
BLADTUT04	bladder tumor, 60 M, match to BLADNOT05	2	0.0253
PLACNOB01	placenta, neonatal F	1	0.0251
LUNGNOT02	lung, 47 M	1	0.0246
TMLR3DT02	lymphocytes (non-adher PBMNC), M/F, 72-hr MLR	1	0.0246
HIPONOT01	brain, hippocampus, 72 F	1	0.0239
RATRNOT02	heart, right atrium, 39 M	1	0.0237
MMLR1DT01	macrophages (adher PBMNC), M/F, 24-hr MLR	1	0.0236

FIGURE 5D

TMLR3DT01	lymphocytes (non-adher PBMNC), M, 96-hr MLR	1	0.0229
PROSNOT06	prostate, 57 M, match to PROSTUT04	2	0.0228
LIVRNOT01	liver, 49 M	1	0.0198
COLNTUT03	colon tumor, 62 M, match to COLNNOT16	1	0.0196
CRBLNOT01	brain, cerebellum, 69 M	1	0.0195
CERVNOT01	cervix, 35 F	1	0.0194
BRSTNOT04	breast, 62 F	2	0.0192
MELANOM01	melanocytes, M, NORM, WM	2	0.0192
LUNGAST01	lung, asthma, 17 M	2	0.0189
SYNOOAT01	synovium, knee, osteoarthritis, 82 F	1	0.0180
MMLR2DT01	macrophages (adher PBMNC), M/F, 48-hr MLR	1	0.0178
SYNORAT04	synovium, wrist, rheumatoid, 62 F	1	0.0174
HNT2NOT01	hNT2 cell line, teratocarcinoma, control	1	0.0173
UCMCL5T01	mononuclear cells, treated IL-5	2	0.0168
CONNNOT01	fat, mesentary, 71 M	1	0.0149
BRSTTUT02	breast tumor, 54 F, match to BRSTNOT03	1	0.0140
BRAITUT01	brain tumor, oligoastrocytoma, 50 F	1	0.0134
SINTFET03	small intestine, fetal F	1	0.0130
KIDNNOT05	kidney, neonatal F	1	0.0106
CORPNOT02	brain, corpus callosum, Alzheimer's, 74 M	1	0.0103
BRSTTUT01	breast tumor, 55 F, match to BRSTNOT02	1	0.0095
LUNGFET03	lung, fetal F	1	0.0091
BRAINOM01	brain, infant F, NORM, WM	1	0.0045

FIGURE 5E